



SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Lonsdale, John
Milner, Peter
Payne, David
Pearson, Stewart

(ii) TITLE OF THE INVENTION: Novel FabI

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SmithKline Beecham Corporation
(B) STREET: 709 Swedeland Road
(C) CITY: King of Prussia
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19406-0939

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 28-August-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/024845
(B) FILING DATE: 28-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Gimmi, Edward R
(B) REGISTRATION NUMBER: 38,891
(C) REFERENCE/DOCKET NUMBER: GM50005

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 610-270-4478

(B) TELEFAX: 610-270-5090

(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Leu Asn Leu Glu Asn Lys Thr Tyr Val Ile Met Gly Ile Ala Asn
 1 5 10 15
 Lys Arg Ser Ile Ala Phe Gly Val Ala Lys Val Leu Asp Gln Leu Gly
 20 25 30
 Ala Lys Leu Val Phe Thr Tyr Arg Lys Glu Arg Ser Arg Lys Glu Leu
 35 40 45
 Glu Lys Leu Leu Glu Gln Leu Asn Gln Pro Glu Ala His Leu Tyr Gln
 50 55 60
 Ile Asp Val Gln Ser Asp Glu Glu Val Ile Asn Gly Phe Glu Gln Ile
 65 70 75 80
 Gly Lys Asp Val Gly Asn Ile Asp Gly Val Tyr His Ser Ile Ala Phe
 85 90 95
 Ala Asn Met Glu Asp Leu Arg Gly Arg Phe Ser Glu Thr Ser Arg Glu
 100 105 110
 Gly Phe Leu Leu Ala Gln Asp Ile Ser Ser Tyr Ser Leu Thr Ile Val
 115 120 125
 Ala His Glu Ala Lys Lys Leu Met Pro Glu Gly Gly Ser Ile Val Ala
 130 135 140
 Thr Thr Tyr Leu Gly Gly Glu Phe Ala Val Gln Asn Tyr Asn Val Met
 145 150 155 160
 Gly Val Ala Lys Ala Ser Leu Glu Ala Asn Val Lys Tyr Leu Ala Leu
 165 170 175
 Asp Leu Gly Pro Asp Asn Ile Arg Val Asn Ala Ile Ser Ala Gly Pro
 180 185 190
 Ile Arg Thr Leu Ser Ala Lys Gly Val Gly Gly Phe Asn Thr Ile Leu
 195 200 205
 Lys Glu Ile Glu Glu Arg Ala Pro Leu Lys Arg Asn Val Asp Gln Val
 210 215 220

Glu Val Gly Lys Thr Ala Ala Tyr Leu Leu Ser Asp Leu Ser Ser Gly
 225 230 235 240
 Val Thr Gly Glu Asn Ile His Val Asp Ser Gly Phe His Ala Ile Lys
 245 250 255

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGTTAAATC TTGAAACAA AACATATGTC ATCATGGGAA TCGCTAATAA GCGTAGTATT	60
GCTTTTGGTG TCGCTAAAGT TTTAGATCAA TTAGGTGCTA AATTAGTATT TACTTACCGT	120
AAAGAACGTA GCCGTAAAGA GCTTGAAAAA TTATTAGAAC AATTAAATCA ACCAGAAGCG	180
CACCTATATC AAATTGATGT TCAAAGCGAT GAAGAGGTTA TTAATGGTTT TGAGCAAAAT	240
GGTAAAGATG TTGGCAATAT TGATGGTGTA TATCATTCOA TCGCATTTGC TAATATGGAA	300
GACTTACGCG GACGCTTTTC TGAACCTTCA CGTGAAGGCT TCTTGTAGC TCAAGACATT	360
AGTTCTTACT CATTAACAAT TGTGGCTCAT GAAGCTAAAA AATTAATGCC AGAAGGTGGT	420
AGCATTGTTG CAACAACATA TTTAGGTGGC GAATTCGCAG TTCAAAATTA TAATGTGATG	480
GGTGTGCTA AAGCGAGCTT AGAAGCAAAT GTTAAATATT TAGCATTAGA CTTAGGTCTT	540
GATAATATTC GCGTTAATGC AATTTCAGCT GGTCCAATCC GTACATTAAG TGCAAAAGGT	600
GTGGGTGGTT TCAATACAAT TCTTAAAGAA ATCGAAGAGC GTGCACCTTT AAAACGTAAC	660
GTGTGATCAAG TAGAAGTAGG TAAACACGCG GCTTACTTCT TAAAGTACTT ATCAAGTGGC	720
GTTACAGGTT AAAATATTCA TGTAGATAGC GGATTCCACG CAATTAAATA A	771